



SEQUENCE LISTING

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<110> Naoyuki TANIGUCHI et al.

<120> ALPHA 1-6 FUCOSYLTRANSFERASE

<130> 2356-7

<140> 09/839,136

<141> 2001-04-23

<150> 09/442,629

<151> 1999-11-18

<150> 08/913,805

<151> 1998-01-07

<150> PCT/JP97/00171

<151> 1997-01-23

<160> 15

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1728

<212> DNA

<213> Pig

<220>

<221> CDS

<222> (1)...(1728)

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gcc tgg ggg acc ttg cta ttt tac ata ggt ggt cac ttg gta cga gat 96
Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
20 25 30
aat gac cac tct gat cac tct agc cga gaa ctg tcc aag att ttg gca 144
Asn Asp His Ser Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
35 40 45
aag ctg gaa cgc tta aaa caa caa aat gaa gac ttg agg aga atg gct 192
Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
50 55 60
gga tct ctc cga ata cca gaa ggc ccc att gat cag ggg cca gct tca 240
Gly Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ser
65 70 75 80
gga aga gtt cgt gct tta gaa gag caa ttt atg aag gcc aaa gaa cag 288

Gly Arg Val Arg Ala Leu Glu Glu Gln Phe Met Lys Ala Lys Glu Gln
85 90 95

att gaa aat tat aag aaa caa act aaa aat ggt cca ggg aag gat cat 336
Ile Glu Asn Tyr Lys Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His
100 105 110

gaa atc cta agg agg agg att gaa aat gga gct aaa gag ctc tgg ttt 384
Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
115 120 125

ttt cta caa agt gag ttg aag aaa tta aag aat tta gaa gga aat gaa 432
Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu
130 135 140

ctc caa aga cat gca gat gaa ttt cta tca gat ttg gga cat cat gaa 480
Leu Gln Arg His Ala Asp Glu Phe Leu Ser Asp Leu Gly His His Glu
145 150 155 160

agg tct ata atg acg gat cta tac tac ctc agt caa aca gat ggg gca 528
Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
165 170 175

ggt gat tgg cgt gaa aag gag gcc aaa gat ctg aca gag ctg gtc cag 576
Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
180 185 190

cgg aga ata aca tat ctt cag aat ccc aag gac tgc agc aaa gcc aag 624
Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys
195 200 205

aag cta gtg tgt aat atc aac aaa ggc tgt ggc tat ggc tgt cag ctc 672
Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
210 215 220

cat cat gta gtg tac tgc ttt atg att gca tat ggc acc cag cga aca 720
His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
225 230 235 240

ctc gcc ttg gaa tct cac aat tgg cgc tac gct act ggg gga tgg gaa 768
Leu Ala Leu Glu Ser His Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
245 250 255

act gtg ttt aga cct gta agt gag acg tgc aca gac aga tct ggc agc 816
Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ser
260 265 270

tcc act gga cat tgg tca ggt gaa gta aag gac aaa aat gtt cag gtg 864
Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
275 280 285

gtt gag ctc ccc att gta gac agt gtt cat cct cgt cct cca tat tta 912
Val Glu Leu Pro Ile Val Asp Ser Val His Pro Arg Pro Pro Tyr Leu
290 295 300

ccc ctg gct gtc cca gaa gac ctt gca gat cga ctt gta cga gtc cat 960

Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His
 305 310 315 320
 ggt gat cct gca gtg tgg tgg gta tcc cag ttt gtc aag tac ttg att 1008
 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
 325 330 335
 cgc cca caa ccc tgg ctg gaa aag gaa ata gaa gag gcc acc aag aag 1056
 Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
 340 345 350
 cta ggc ttc aaa cat cca gtt att gga gtc cat gtt aga cgc aca gac 1104
 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
 355 360 365
 aaa gtg gga gcg gaa gca gcc ttc cat ccc att gag gaa tac acg gtg 1152
 Lys Val Gly Ala Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Thr Val
 370 375 380
 cac gtt gaa gaa gac ttt cag ctt ctt gct cgc aga atg caa gtg gat 1200
 His Val Glu Glu Asp Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
 385 390 395 400
 aaa aaa agg gtg tat ttg gcc aca gat gac cct gct ttg tta aaa gag 1248
 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys Glu
 405 410 415
 gca aaa aca aag tac ccc agt tat gaa ttt att agt gat aac tct atc 1296
 Ala Lys Thr Lys Tyr Pro Ser Tyr Glu Phe Ile Ser Asp Asn Ser Ile
 420 425 430
 tct tgg tca gct gga cta cat aat cga tat aca gaa aat tca ctt cgg 1344
 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
 435 440 445
 ggt gtg atc ctg gat ata cac ttt ctc tcc cag gca gac ttc cta gtg 1392
 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
 450 455 460
 tgt act ttt tca tcg cag gtc tgt aga gtt gct tat gaa atc atg caa 1440
 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
 465 470 475 480
 gcg ctg cat cct gat gcc tct gcg aac ttc cgt tct ttg gat gac atc 1488
 Ala Leu His Pro Asp Ala Ser Ala Asn Phe Arg Ser Leu Asp Asp Ile
 485 490 495
 tac tat ttt gga ggc cca aat gcc cac aac caa att gcc att tat cct 1536
 Tyr Tyr Phe Gly Gly Pro Asn Ala His Asn Gln Ile Ala Ile Tyr Pro
 500 505 510
 cac caa cct cga act gaa gga gaa atc ccc atg gaa cct gga gat att 1584
 His Gln Pro Arg Thr Glu Gly Glu Ile Pro Met Glu Pro Gly Asp Ile
 515 520 525
 att ggt gtg gct gga aat cac tgg gat gcc tat cct aaa ggt gtt aac 1632

Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Pro Lys Gly Val Asn
 530 535 540

aga aaa ctg gga agg acg ggc cta tat ccc tcc tac aaa gtt cga gag 1680
 Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
 545 550 555 560

aag ata gaa aca gtc aag tac ccc aca tat ccc gag gct gac aag taa 1728
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 565 570 575

<210> 2
 <211> 575
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 <213> Pig

<400> 2
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 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
 20 25 30
 Asn Asp His Ser Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
 35 40 45
 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
 50 55 60
 Gly Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ser
 65 70 75 80
 Gly Arg Val Arg Ala Leu Glu Glu Gln Phe Met Lys Ala Lys Glu Gln
 85 90 95
 Ile Glu Asn Tyr Lys Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His
 100 105 110
 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
 115 120 125
 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu
 130 135 140
 Leu Gln Arg His Ala Asp Glu Phe Leu Ser Asp Leu Gly His His Glu
 145 150 155 160
 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
 165 170 175
 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
 180 185 190
 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys
 195 200 205
 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
 210 215 220
 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
 225 230 235 240
 Leu Ala Leu Glu Ser His Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
 245 250 255
 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ser
 260 265 270
 Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
 275 280 285
 Val Glu Leu Pro Ile Val Asp Ser Val His Pro Arg Pro Pro Tyr Leu

290	295	300
Pro Leu Ala Val	Pro Glu Asp Leu Ala Asp Arg	Leu Val Arg Val His
305	310	315
Gly Asp Pro Ala Val	Trp Trp Val Ser Gln Phe Val	Lys Tyr Leu Ile
325	330	335
Arg Pro Gln Pro Trp	Leu Glu Lys Glu Ile Glu Glu Ala Thr	Lys Lys
340	345	350
Leu Gly Phe Lys His	Pro Val Ile Gly Val His Val Arg Arg Thr	Asp
355	360	365
Lys Val Gly Ala Glu	Ala Ala Phe His Pro Ile Glu Glu Tyr Thr	Val
370	375	380
His Val Glu Glu Asp	Phe Gln Leu Leu Ala Arg Arg Met Gln Val	Asp
385	390	395
Lys Lys Arg Val Tyr	Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys	Glu
405	410	415
Ala Lys Thr Lys Tyr	Pro Ser Tyr Glu Phe Ile Ser Asp Asn Ser	Ile
420	425	430
Ser Trp Ser Ala Gly	Leu His Asn Arg Tyr Thr Glu Asn Ser Leu	Arg
435	440	445
Gly Val Ile Leu Asp	Ile His Phe Leu Ser Gln Ala Asp Phe Leu	Val
450	455	460
Cys Thr Phe Ser Ser	Gln Val Cys Arg Val Ala Tyr Glu Ile Met	Gln
465	470	475
Ala Leu His Pro Asp	Ala Ser Ala Asn Phe Arg Ser Leu Asp Asp	Ile
485	490	495
Tyr Tyr Phe Gly Gly	Pro Asn Ala His Asn Gln Ile Ala Ile Tyr	Pro
500	505	510
His Gln Pro Arg Thr	Glu Gly Glu Ile Pro Met Glu Pro Gly Asp	Ile
515	520	525
Ile Gly Val Ala Gly	Asn His Trp Asp Gly Tyr Pro Lys Gly Val	Asn
530	535	540
Arg Lys Leu Gly Arg	Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg	Glu
545	550	555
Lys Ile Glu Thr Val	Lys Tyr Pro Thr Tyr Pro Glu Ala Asp	Lys
565	570	575

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Primer

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 Arg Ile Glu Asn Gly Ala Lys Glu Leu Gln
 20 25

<210> 4
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Primer

<400> 4
Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys
1 5 10

<210> 5
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
Lys Tyr Leu Ile Arg Pro Gln Pro Trp Leu Glu Lys
1 5 10

<210> 6
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Primer

<400> 6
Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys
1 5 10

<210> 7
<211> 20
<212> DNA
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<220>
<223> Primer

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<222> 9, 18
<223> n = A,T,C or G

<221> misc_feature
<222> 9, 18
<223> n = A,T,C or G

<400> 7
aarsaraacna araaygggcc

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<210> 8
<211> 20
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<220>

<223> Primer

<221> misc_feature

<222> 3, 9, 12

<223> n = A,T,C or G

<221> misc_feature

<222> 3, 9, 12

<223> n = A,T,C or G

<400> 8

tonggrtang tnggrtaytt

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<210> 9

<211> 2100

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (198)...(1925)

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agagaataat ttgtctgaag catcatgtgt tgaaacaaca gaagtctatt cacctgtgca 120
ctaactagaa acagagttac aatgttttca attctttgag ctccaggact ccaggggaagt 180
gagttgaaaa tctgaaa atg cgg cca tgg act ggt tcc tgg cgt tgg att 230
Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile
1 5 10

atg ctc att ctt ttt gcc tgg ggg acc ttg ctg ttt tat ata ggt ggt 278
Met Leu Ile Leu Phe Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly
15 20 25

cac ttg gta cga gat aat gac cat cct gat cac tct agc cga gaa ctg 326
His Leu Val Arg Asp Asn Asp His Pro Asp His Ser Ser Arg Glu Leu
30 35 40

tcc aag att ctg gca aag ctt gaa cgc tta aaa cag cag aat gaa gac 374
Ser Lys Ile Leu Ala Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp
45 50 55

ttg agg cga atg gcc gaa tct ctc cgg ata cca gaa ggc cct att gat 422
Leu Arg Arg Met Ala Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp
60 65 70 75

cag ggg cca gct ata gga aga gta cgc gtt tta gaa gag cag ctt gtt 470
Gln Gly Pro Ala Ile Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val
80 85 90

aag gcc aaa gaa cag att gaa aat tac aag aaa cag acc aga aat ggt 518
Lys Ala Lys Glu Gln Ile Glu Asn Tyr Lys Lys Gln Thr Arg Asn Gly
95 100 105

ctg ggg aag gat cat gaa atc ctg agg agg agg att gaa aat gga gct 566
 Leu Gly Lys Asp His Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala
 110 115 120

aaa gag ctc tgg ttt ttc cta cag agt gaa ttg aag aaa tta aag aac 614
 Lys Glu Leu Trp Phe Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn
 125 130 135

tta gaa gga aat gaa ctc caa aga cat gca gat gaa ttt ctt ttg gat 662
 Leu Glu Gly Asn Glu Leu Gln Arg His Ala Asp Glu Phe Leu Leu Asp
 140 145 150 155

tta gga cat cat gaa agg tct ata atg acg gat cta tac tac ctc agt 710
 Leu Gly His His Glu Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser
 160 165 170

cag aca gat gga gca ggt gat tgg cgg gaa aaa gag gcc aaa gat ctg 758
 Gln Thr Asp Gly Ala Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu
 175 180 185

aca gaa ctg gtt cag cgg aga ata aca tat ctt cag aat ccc aag gac 806
 Thr Glu Leu Val Gln Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp
 190 195 200

tgc agc aaa gcc aaa aag ctg gtg tgt aat atc aac aaa ggc tgt ggc 854
 Cys Ser Lys Ala Lys Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly
 205 210 215

tat ggc tgt cag ctc cat cat gtg gtc tac tgc ttc atg att gca tat 902
 Tyr Gly Cys Gln Leu His His Val Val Tyr Cys Phe Met Ile Ala Tyr
 220 225 230 235

ggc acc cag cga aca ctc atc ttg gaa tct cag aat tgg cgc tat gct 950
 Gly Thr Gln Arg Thr Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala
 240 245 250

act ggt gga tgg gag act gta ttt agg cct gta agt gag aca tgc aca 998
 Thr Gly Gly Trp Glu Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr
 255 260 265

gac aga tct ggc atc tcc act gga cac tgg tca ggt gaa gtg aag gac 1046
 Asp Arg Ser Gly Ile Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp
 270 275 280

aaa aat gtt caa gtg gtc gag ctt ccc att gta gac agt ctt cat ccc 1094
 Lys Asn Val Gln Val Val Glu Leu Pro Ile Val Asp Ser Leu His Pro
 285 290 295

cgt cct cca tat tta ccc ttg gct gta cca gaa gac ctc gca gat cga 1142
 Arg Pro Pro Tyr Leu Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg
 300 305 310 315

ctt gta cga gtg cat ggt gac cct gca gtg tgg tgg gtg tct cag ttt 1190
 Leu Val Arg Val His Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe
 320 325 330

gtc aaa tac ttg atc cgc cca cag cct tgg cta gaa aaa gaa ata gaa	1238
Val Lys Tyr Leu Ile Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu	
335 340 345	
gaa gcc acc aag aag ctt ggc ttc aaa cat cca gtt att gga gtc cat	1285
Glu Ala Thr Lys Lys Leu Gly Phe Lys His Pro Val Ile Gly Val His	
350 355 360	
gtc aga cgc aca gac aaa gtg gga aca gaa gct gcc ttc cat ccc att	1334
Val Arg Arg Thr Asp Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile	
365 370 375	
gaa gag tac atg gtg cat gtt gaa gaa cat ttt cag ctt ctt gca cgc	1382
Glu Glu Tyr Met Val His Val Glu Glu His Phe Gln Leu Leu Ala Arg	
380 385 390 395	
aga atg caa gtg gac aaa aaa aga gtg tat ttg gcc aca gat gac cct	1430
Arg Met Gln Val Asp Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro	
400 405 410	
tct tta tta aag gag gca aaa aca aag tac ccc aat tat gaa ttt att	1478
Ser Leu Leu Lys Glu Ala Lys Thr Lys Tyr Pro Asn Tyr Glu Phe Ile	
415 420 425	
agt gat aac tct att tcc tgg tca gct gga ctg cac aat cga tac aca	1526
Ser Asp Asn Ser Ile Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr	
430 435 440	
gaa aat tca ctt cgt gga gtg atc ctg gat ata cat ttt ctc tct cag	1574
Glu Asn Ser Leu Arg Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln	
445 450 455	
gca gac ttc cta gtg tgt act ttt tca tcc cag gtc tgt cga gtt act	1622
Ala Asp Phe Leu Val Cys Thr Phe Ser Ser Gln Val Cys Arg Val Thr	
460 465 470 475	
tat gaa att atg caa aca cta cat cct gat gcc tct gca aac ttc cat	1670
Tyr Glu Ile Met Gln Thr Leu His Pro Asp Ala Ser Ala Asn Phe His	
480 485 490	
tct tta gat gac atc tac tat ttt ggg ggc cag aat gcc cac aat caa	1718
Ser Leu Asp Asp Ile Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln	
495 500 505	
att gcc att tat gct cac caa ccc cga act gca gat gaa att ccc atg	1766
Ile Ala Ile Tyr Ala His Gln Pro Arg Thr Ala Asp Glu Ile Pro Met	
510 515 520	
gaa cct gga gat atc att ggt gtg gct gga aat cat tgg gat ggc tat	1814
Glu Pro Gly Asp Ile Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr	
525 530 535	
tct aaa ggt gtc aac agg aaa ttg gga agg acg ggc cta tat ccc tcc	1862
Ser Lys Gly Val Asn Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser	
540 545 550 555	

tac aaa gtt cca gag aag ata gaa acg gtc aag tac ccc aca tat cct 1910
 Tyr Lys Val Pro Glu Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro
 560 565 570

gag gct gag aaa taa agctcacatg gaagagataa acgaccaaac tcagttcgac 1965
 Glu Ala Glu Lys *
 575

caaaactcagt tcaaaaccatt tcagccaaac tgtagatgaa gagggctctg atctaacaaa 2025
 ataagggttat atgagtagat actctcagca ccaagagcag ctgggaactg acataggctt 2085
 caattgggtgg aattc 2100

<210> 10
 <211> 575
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
 35 40 45
 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
 50 55 60
 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ile
 65 70 75 80
 Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
 85 90 95
 Ile Glu Asn Tyr Lys Lys Gln Thr Arg Asn Gly Leu Gly Lys Asp His
 100 105 110
 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
 115 120 125
 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu
 130 135 140
 Leu Gln Arg His Ala Asp Glu Phe Leu Leu Asp Leu Gly His His Glu
 145 150 155 160
 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
 165 170 175
 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
 180 185 190
 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys
 195 200 205
 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
 210 215 220
 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
 225 230 235 240
 Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
 245 250 255
 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ile
 260 265 270
 Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
 275 280 285
 Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu

290	295	300
Pro Leu Ala Val	Pro Glu Asp Leu Ala Asp	Arg Leu Val Arg Val His
305	310	315
Gly Asp Pro Ala Val	Trp Trp Val Ser Gln Phe Val	Lys Tyr Leu Ile
325	330	335
Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile	Glu Glu Ala Thr Lys Lys	
340	345	350
Leu Gly Phe Lys His Pro Val Ile Gly Val	His Val Arg Arg Thr Asp	
355	360	365
Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile	Glu Glu Tyr Met Val	
370	375	380
His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg	Met Gln Val Asp	
385	390	395
Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp	Pro Ser Leu Leu Lys Glu	
405	410	415
Ala Lys Thr Lys Tyr Pro Asn Tyr Glu Phe Ile	Ser Asp Asn Ser Ile	
420	425	430
Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr	Glu Asn Ser Leu Arg	
435	440	445
Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp	Phe Leu Val	
450	455	460
Cys Thr Phe Ser Ser Gln Val Cys Arg Val Thr Tyr Glu Ile	Met Gln	
465	470	475
Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp	Asp Ile	
485	490	495
Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Ile	Tyr Ala	
500	505	510
His Gln Pro Arg Thr Ala Asp Glu Ile Pro Met Glu Pro Gly Asp	Ile	
515	520	525
Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Val	Asn	
530	535	540
Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Pro	Glu	
545	550	555
Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys		
565	570	575

<210> 11
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 11
 Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ile Gly
 1 5 10

<210> 12
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 <212> PRT
 <213> Artificial Sequence

<220>

<213> Primer

<400> 12

Lys Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr
1 5 10 15
Asp Lys Val Gly Thr Cys Ala Ala Phe
20 25

<210> 13

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Primer

<400> 13

Thr Lys Tyr Pro Asn Tyr Glu Phe Ile Ser Asp Asn Ser
1 5 10

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 14

ttyaarcayc chgtbatygg

20

<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Primer

<400> 15

gwrtrtrcrg wratraaytc

20